

**REMARKS/ARGUMENTS**

By this preliminary amendment, Applicant amends the specification, claims, and drawings. The specification is amended to include Sequence No. identifiers and paragraph numbers. For the sake of clarity, Applicant has introduced these amendments by way of providing a substitute specification. Both a clean copy and a marked up version of the specification are provided.


The drawings have also been amended to include Sequence No. identifiers.

Claims 5-7, 11, 14, 15, 17, 19, 21, 23, 25, 27-36, 38-42, 49-53 are amended to remove improper multiple dependencies. Claims 15-26 have been amended to show the Sequence ID No. indication. Claims 1-54 are pending in the application.

No new matter is introduced by the amendments. Applicant respectfully requests entry of this preliminary amendment prior to examination on the merits.

Respectfully submitted,

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**Amendments to the Drawings:**

The attached sheet of drawings includes changes to Figs. 1-9. This sheet, which includes Figs. 1-9, replaces the original sheets included Figs. 1-9. In Figs. 1-9, Sequence ID No. identifiers been added.

Attachment: Replacement Sheet  
Annotated Sheet Showing Changes



1/9

Fig. 1

E V Q L L E Q P G A  
GAGGTGCAGCTGCTCGAGCAGCCTGGGGCT 30  
E L A K P G A S V K  
GAACTGGCAAAACCTGGGGCCTCAGTGAAG 60  
M S C K A S G Y T F  
ATGTCCTGCAAGGCTTCTGGCTACACCTTT 90  
T N Y W I H W V K Q  
ACTAACTACTGGATTCACTGGGGTGAAACAG 120  
R P G Q G L K W I G  
AGGCCTGGACAGGGTCTGAAATGGATTGGA 150  
Y I N P A T G S T S  
TACATTAATCCTGCCACTGGTTCCACTTCT 180  
Y N Q D F Q D R A T  
TACAATCAGGACTTTCAGGACAGGGCCACT 210  
L T A D K S S T T A  
TTGACCGCAGACAAGTCCTCCACCACAGCC 240  
Y M Q L T S L T S E  
TACATGCAGCTGACCAGCCTGACATCTGAG 270  
D S S V Y Y C A R E  
GACTCTTCAGTCTATTACTGTGCAAGAGAG 300  
G Y D G F D S W G Q  
GGGTACGACGGGTTTGACTCCTGGGGGCCAA 330  
G T T L T V S S  
GGCACCACTCTCACAGTCTCCTCA 360

SEQ ID NO. 1

2/9

Fig. 2

E L V L T Q S P A I  
GAGCTCGTGCTCACCCAGTCTCCAGCAATC 30  
M S A S P G E K V T  
ATGTCTGCATCTCCAGGGGAGAAGGTCACC 60  
M T C S A S S S V N  
ATGACCTGCAGTGCCAGCTCAAGTGTAAT 90  
Y M Y W Y Q Q K S G  
TACATGTACTTGGTACCAGCAGAAAGTCAGGC 120  
T S P K R W I Y D T  
ACCTCCCCCAAAGATGGATTTATGACACA 150  
S K L A S G V P A R  
TCCAAATTGGCTTCTTGGAGTCCCTGCTCGC 180  
F S G S G S G T S Y  
TTCAGTGGCAGTGGGTCTGGGACCTCTTAC 210  
S L T L S S M E A E  
TCTCTCACACTCAGCAGCATGGAGGCTGAA 240  
D A A T Y Y C Q Q W  
GATGCCGCCACTTATTACTGCCCAGCAGTGG 270  
S S N P Y T F G G G  
AGTAGTAATCCGTACACGTTCGGAGGGGGG 300  
T K L E I K  
ACCAAGCTGGAGATAAAA 330

SEQ ID NO. 2

Fig. 3

+1 E V Q L Q Q S G A E  
GAGGTTTCAGCTGCAGCAGTCTGGGGGCAGAG 30

+1 L V K P G A S V K L  
CTTGTGAAGCCTGGGGGCCTCAGTCAAGTTG 60

+1 S C T S S G F N I K  
TCCTGCACATCTTCTGGCTTCAACATTAAA 90

+1 D T Y V H W M K Q R  
GACACCTATGTGCACTTGGATGAAACAGAGG 120

+1 P E Q G L E W I G K  
CCTGAACAGGGCCTGGAGTGGATTGGAAAG 150

+1 I D P A N G K T K Y  
ATTGATCCTGCGAATGGTAAAACTAAATAT 180

+1 D P I F Q A K A T M  
GACCCGATATTCCAGGCCAAGGCCACTATG 210

+1 T A D A S S N T A Y  
ACAGCAGACGCATCCTCCAATACAGCCTAC 240

+1 L Q L S S L T S E D  
CTGCAACTCAGCAGCCTGACTTCTGAGGAC 270

+1 T A V Y Y C A L P I  
ACTGCCGTCTATTACTGTGCTCTCCCCATT 300

+1 Y Y A S S W F A Y W  
TATTACGCTAGTTCCTGGTTTGTCTTACTGG 330

+1 G Q G T L V T V S A  
GGCCAAGGGACTCTGGTCACTGTCTCTGCA 360

SEQ ID NO. 3

Fig. 4

+1 D I V M T Q S H K F  
GACATTGTGATGACCCAGTCTCACAAATTC 30

+1 M S T S V G D R V S  
ATGTCCACATCAGTAGGAGACAGGGTTCAGC 60

+1 I T C K A S Q D V G  
ATCACCTGCAAGGCCAGTCAGGATGTGGGT 90

+1 T S V A W Y Q Q K P  
ACTTCTGTTGCCTTGGTATCAACAGAAACCT 120

+1 G H S P K L L I Y W  
GGGCACTCTCCTAAATTACTGATTTACTTGG 150

+1 T S T R H T G V P D  
ACATCCACCCGGCACACTTGGAGTCCCTGAT 180

+1 R F T G S G S G T D  
CGCTTCACAGGCAGTGGATCTGGGACAGAT 210

+1 F I L T I S N V Q S  
TTCATTCTCACCATTAGCAATGTGCAGTCT 240

+1 E D L A D Y F C Q Q  
GAAGACTTGGCAGATTATTTCTGTCAGCAA 270

+1 Y S S S P T F G G G  
TATAGCAGCTCTCCCACGTTCGGAGGGGGG 300

+1 A K V E I K  
GCCAAGGTGGAAATAAAA 330

SEQ ID NO. 4

5/9

+1 D I L L T Q S P A I L S V S P G E  
GACATCTTGC TGA CT CAGTC TCCAGCCATC CTGTCTGTGA GTCCAGGAGA 50  
+1 R V S F S C R A S Q S I G T R I H  
AAGAGTCAGT TTCTCCTGCA GGGCCAGTCA GAGCATTGGC ACAAGAATAC 100  
+1 W Y Q Q R T N G S P R L L I K Y  
ACTGGTATCA ACAAAGAACA AATGGTTCTC CAAGGCTTCT CATAAAGTAT 150  
+1 G S E S I S G I P S R F S G S G S  
GGTTCTGAGT CTATCTCTGG GATCCCTTCC AGGTTTAGTG GCAGTGGATC 200  
+1 G T D F S L S I N S V E S E D I A  
AGGGACAGAT TTAGTCTTA GCATCAACAG TGTCGAGTCT GAAGATATTG 250  
+1 D Y Y C Q Q S N T W P L T F G A  
CAGATTATTA CTGT CAACAA AGTAATACCT GGCCGCTCAC GTTCGGTGCT 300  
+1 G T K L E L K  
GGGACCAAGC TGGAGCTGAA A 350

Fig. 5

SEQ ID NO. 5

+1 E V Q L L E Q S G A E L V K P G A  
GAGTGCAGC TGCTCGAGCA GTCTGGAGCT GAGCTGGTGA AGCCTGGGGC 50  
+1 S V K I S C K A S G Y A F S T S W  
CTCAGTGAAG ATTTCTTGCA AGGCTTCTGG CTACGCATTC AGTACCTCCT 100  
+1 M N W V K Q R P G K G L E W I G  
GGATGAAC TG GGTGAAACAG AGGCCTGGAA AGGTCTTGA GTGGATTGGA 150  
+1 R I Y P G D G D T N Y N G K F K G  
CGGATTATC CTGGAGATGG AGATACTAAC TACAATGGGA AGTTCAAGGG 200  
+1 K A T L T A D K S S S T A Y M Q L  
CAAGGCCACA CTGACTGCAG ACAATCCTC CAGCACAGCC TACATGCAAC 250  
+1 N S L T S E D S A V Y F C V R E  
TCAACAGCCT GACATCTGAG GACTCTGCGG TCTACTTCTG TGTAAGA GAG 300  
+1 D A Y Y S N P Y S L D Y W G Q G T  
GATGCCCTATT ATAGTAACCC CTATAGTTTG GACTAC TGGG GTCAAGGAAC 350  
+1 S V T V S S  
CTCAGTCACC GTCTCCTCA 400

Fig. 6

SEQ ID NO. 6



7/9

+1 E L Q M T Q S P S S L S A S L G D  
GAGCTCCAGA TGACCCAGTC TCCATCCAGT CTGTCTGCAT CCCTTGGAGA 50  
+1 T I T I T C H A S Q N I N V W L S  
CACAATTACC ATCACTTGC C ATGCCAGTCA GAACATTAAAT GTTTGGTTAA 100  
+1 W Y Q Q K P G D I P K L L I Y K  
GCTGGTATCA GCAGAAACCA GGAGATATCC CTAACCTATT GATCTATAAG 150  
+1 A S N L H T G V P S R F S G S G S  
GCTTCCAACT TGCACACAGG CGTCCCATCA AGGTTTAGTG GCAGTGGATC 200  
+1 G T G F T L V I S S L Q P E D I A  
TGGAACAGGT TTCACATTAG TCATCAGCAG CCTGCAGCCT GAAGACATTG 250  
+1 T Y Y C Q Q G R S Y P L T F G A  
CCACTTACTA CTGTCAACAG GGTCCGAAGTT ATCCTCTCAC GTTCGGTGCT 300  
+1 G T K L E L K  
GGGACCAAGC TGGAGCTGAA A 350

Fig. 7

SEQ ID NO. 7

~~6/9~~ 8/9

+1 E V Q L L E E S G G G L V K P G G  
GAGGTGCAGC TGCTCGAGGA GTCTGGGGGA GGCTTAGTGA AGCCTGGAGG 50  
+1 S L Q L S C S A S G F T F S S H F  
GTCCCTGCAA CTCTCCTGTT CAGCCTCTGG ATTCACTTTC AGTAGCCATT 100  
+1 M S W V R Q T P E K R L E W V A  
TCATGTCT TG GGTTCGCCAA ACTCCAGAGA AGAGGCTGGA GTGGGTCGCA 150  
+1 S I S S G G D S F Y P D S L K G R  
TCCATTAGTA GTGGTGGTGA CAGTTTCTAT CCAGACAGTC TGAAGGGCCG 200  
+1 F A I S R D N A R N I L F L Q M S  
ATTCGCCATC TCCAGAGATA ATGCCAGGAA CATCCTGTTC CTGCAAATGA 250  
+1 S L R S E D S A M Y F C T R D Y  
GCAGTCTGAG GTCTGAGGAC TCGGCCATGT ATTTCTGTAC AAGA GACTAC 300  
+1 S W Y A L D Y W G Q G T S V T V S  
TCTTGGTATG CTTTGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC 350  
+1 S

400

SEQ ID NO: 8

CTCA

9/9

Fig. 9

